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The association of *CYP2C9* gene polymorphisms with colorectal carcinoma in Han Chinese

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Abstract

Background: Cytochrome P450 (CYP) 2C9 is an important enzyme involved in xenobiotics metabolism. This study investigated the association of *CYP2C9* gene coding region polymorphisms with colorectal cancer (CRC) in Chinese Han population.
Methods: Four hundred and eighty-three healthy controls and 286 sporadic CRC patients participated in this study. Direct sequencing was used to identify the sequence polymorphisms.
Results: We detected the significant association of 2 coding region SNPs, rs1057910 and rs1057911, of *CYP2C9* with the risk of developing sporadic CRC for Han Chinese. These 2 SNPs showed a strong linkage disequilibrium (LD) ($r^2=0.97$, $D'=0.985$). Significantly different minor allele frequencies were found for SNPs rs1057910 and rs1057911 between the cases (7% and 7.2%, respectively) and controls (3% and 2.9%, respectively) with adjusted $P=0.0004$ and 0.0002, respectively. Individuals heterozygous for rs1057910A/C or rs1057911A/T showed 2.589-fold (95% CI: 1.549–4.330) or 2.770-fold (95% CI 1.653–4.643) increased risk of developing sporadic CRC. We did not detect any homozygote minor allele carrier for either rs1057910 or rs1057911 in our study population. The CRC association appeared to be more evident for individuals over age 50 y, for men, and for rectum cancer site.
Conclusion: There is an association of *CYP2C9* coding region polymorphisms with the risk of developing CRC in Han Chinese after genotyping cases and controls recruited from different locations in China.

Keywords: CYP2C9; SNP; Chinese; Colorectal carcinoma

1. Introduction

Colorectal cancer (CRC) is a major cause of cancer deaths in developed regions worldwide. The marked regional differences of CRC incidence rates implicate the combined influence of genetic predisposition and local environmental factors such as carcinogen exposure and diet [1–3]. Both *in vivo* and *in vitro* studies suggested that the exposure to dietary carcinogens significantly increased CRC risk [4,5]. Cytochrome P450 (CYP) enzymes play key roles in the metabolism of xenobiotics. The CYP2C subfamily, with CYP2C9 as its most abundant member, accounts for about 20% of the total CYP enzymes in human liver [6,7]. CYP2C9 is involved in the

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